

Supplemental Table 2. Differentially expressed total liver proteins of K8-null mice

Spot #	Accession #	Protein ID	Ratio of change	Properties
199	P57780	alpha actinin 4	+1.74	
279	Q9HCE2	KIAA1630 protein	+1.50	anchor actin
317	P17515	valosin-containing protein	+1.71	unknown
563a	Q62357	transferrin	+1.34	
563b	Q62357	transferrin	+1.28	
691	P14824	Annexin A6	+1.29	phospholipid binding
725	P14733	Lamin B1	+1.51	nucleus
801	Q9QXE0	2-hydroxyphytanoyl-CoA lyase	+1.40	
838a	P11983	T-complex protein 1	+1.20	chaperone/cytoplasmic
838b	P11983	T-complex protein 1	+1.36	chaperone/cytoplasmic
872	NP_031663	Chaperonin subunit 5	+1.26	chaperone
874a	Q8BXM3	ALDH4A1	+2.78	mitochondria
874b	Q8BXM3	ALDH4A1	-1.12	mitochondria
874c	Q8BXM3	ALDH4A1	-1.28	mitochondria
874d	Q8BXM3	ALDH4A1	-1.47	mitochondria
896	P34914	Soluble epoxide hydrolase	-1.22	cytoplasmic
936	P02551	Tubulin alpha-1	+1.46	
979	P54869	3-HMG-CoA synthase	+1.21	mitochondria, cholesterol, lipid synthesis
999a	P11679	Keratin 8	-20.4	IF protein
999b	P11679	Keratin 8	-2.68	IF protein
999c	P11679	Keratin 8	-6.21	IF protein
999d	P11679	Keratin 8	-2.31	IF protein
1036a	Q03265	ATP synthase, alpha subunit	+2.23	mitochondria
1036b	Q03265	ATP synthase, alpha subunit	+1.41	mitochondria
1071a	P11679	Keratin 8	-4.13	IF protein
1071b	P11679	Keratin 8	-2.45	IF protein
1150a	P05784	Keratin 18	-3.01	IF protein
1150b	P05784	Keratin 18	-3.57	IF protein
1150c	P05784	Keratin 18	-4.56	IF protein
1160	P62192	Proteasome 26S	-1.53	cytoplasmic and nuclear
		ATPase subunit 4		
1180a	P54869	HMG-CoA synthase	-1.40	
1180b	P54869	HMG-CoA synthase	-1.09	
1194	P00966	Argininosuccinate synthetase 1	-1.38	Citrulline-Asp ligase
1235	P29785	Ornithine aminotransferase	+1.30	mitochondria
1261		Endo A' keratin	+1.45	
1268	P19001	Keratin 19	-1.77	
1302a	P60712	beta-actin	+1.66	cytoplasmic and mt
1302b	P60712	beta-actin	+1.59	cytoplasmic and mt
1302c	P60712	beta-actin	+1.43	cytoplasmic and mt
1339a		Lamin receptor 1	-1.34	
1339b		Lamin receptor 1	-1.20	
1391	NP_059066	Haptoglobin	+1.58	reducing renal oxidative damage
1459a	Q61176	Arginase 1	-1.47	cytoplasmic
1459b	Q61176	Arginase 1	+1.52	cytoplasmic

1464	P28474	alcohol dehydrogenase class III	+1.23	cytoplasmic catalyze oxidation
1599	P45376	Aldose reductase	- 1.29	mitochondria
1658	NP_034401	Glycerol phosphate dehydrogenase 1	- 1.53	soluble, mt
1660	Q8C7H3	Albumin 1/alpha-fetoprotein	+4.96	
1714	Q9QXF8	Glycine N-methyltransferase	- 1.21	cytoplasmic
1732	Q9QXF8	Glycine N-methyltransferase	- 1.54	cytoplasmic
1756a	O70251	Elongation factor 1-beta	+1.87	
1756b	O70251	Elongation factor 1-beta	+1.97	
1793	P46952	3-hydroxyanthranilate 3,4-dioxygenase	- 1.36	cytoplasmic
1805	P97429	Annexin A4	+1.33	membrane
1850	P30115	Glutathione S-transferase Yc	+1.53	cytoplasmic
1937	P67778	Prohibitin	+1.32	cytoplasmic, mt
1968	P67778	Prohibitin	+1.32	cytoplasmic, mt
2012a	P16015	Carbonic anhydrase III	- 1.25	cytoplasmic
2012b	P16015	Carbonic anhydrase III	- 1.28	cytoplasmic
2012c	P16015	Carbonic anhydrase III	- 1.19	cytoplasmic
2062	P17751	Triosephosphate isomerase	- 1.26	
2095a	P10649	Glutathione S-transferase Mu 1	+1.15	cytoplasmic
2095b	P10649	Glutathione S-transferase Mu 1	+1.41	cytoplasmic
2121	NP_079650	Glyoxalase	- 1.29	
2251	P29391	Ferritin L chain	+1.80	
2290a	P11589	Major urinary Proteins 2	- 2.17	secreted
2290b	P11589	Major urinary Proteins 2	- 1.76	secreted
